

(FILE 'HOME' ENTERED AT 15:29:41 ON 13 JUL 2004)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE' ENTERED AT 15:29:57 ON 13 JUL 2004

L1 59601 S HBV OR HBSAG
L2 95925 S L1 OR (HEPATITIS B VIRUS)
L3 852 S L2 AND (ESCAPE OR IMMUN?)
L4 852 S L3 AND ESCAPE?
L5 595 S L4 AND (MUTATION? OR VARIANT?)
L6 97 S L5 AND (130 OR 131 OR 133 OR 145)
L7 40 DUP REM L6 (57 DUPLICATES REMOVED)
L8 2 S L7 AND 130

FILE 'GENBANK' ENTERED AT 15:44:20 ON 13 JUL 2004

SET NOTICE DISPLAY 1
SET NOTICE LOGIN DISPLAY

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE' ENTERED AT 15:44:40 ON 13 JUL 2004

L9 62 S L2 AND (MUTATION) AND 130
L10 24 DUP REM L9 (38 DUPLICATES REMOVED)
L11 7480 S L2 AND (NEGATIVE) AND (HBSAG)
L12 771 S L11 AND (MUTATION? OR VARIA?)
L13 10 S L12 AND 130
L14 6 DUP REM L13 (4 DUPLICATES REMOVED)

=>

L7 ANSWER 18 OF 40 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1998:685735 CAPLUS

DOCUMENT NUMBER: 130:37043

TITLE: Patterns of circulating hepatitis B surface antigen **variants** among vaccinated children born to hepatitis B surface antigen carrier and non-carrier mothers. A population-based comparative study

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CORPORATE SOURCE: Div. Epidemiology Public Health, Inst. Biomedical Sciences, Academia Sinica, Taipei, 11529, Taiwan

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AB **Hepatitis B virus (HBV)**

variants that possessed missense **mutation** within the neutralization epitope of the major S antigen as defined by amino acid residues 124-147, termed the "a" determinant **variants**, were identified through a population-based sero-survey of 2305 children of the vaccinated birth cohorts born after 1986. Data on the 678 nucleotides encoding the S antigen of **HBV** were available for 75 **HBV** strains that were collected from 63 vaccinated children and 12 unvaccinated or incompletely vaccinated children, and 21 **HBV** strains from 25 unvaccinated adults. Among the diverse patterns of 1-three amino acid substitutions within the "a" determinant, 145 -Arg occurred most frequently (5/14); other **variants** were: 126-Ala, 127-Thr, 126-Ser/131-Asn/133-Thr, 129-His, 129-Arg, 123-Asn/131-Ile, 133-Leu, 141-Glu, and 141-Arg/144-Ala. Only one of these **variants** occurred in the 16 hepatitis B surface antigen (**HBsAg**)-carrier children born to **HBsAg**-neg. mothers, whereas 12 of these **variants** occurred in the 20 (50%) children born to **HBsAg**-pos. mothers. Early administration of **HBV** vaccine within the neonatal period increased the likelihood of the emergence of these **variants** to 64.7% (11/17). Five of the 21 (23.8%) unvaccinated **HBsAg**-carrier adults harbored the "a" determinant **variants** possessing **mutations** within 125-136, i.e. the putative 1st loop formed by the Cys disulfide bonds. Vaccinated children were likely to harbor **HBV variants** possessing **mutations** involving altered charge of side chains and/or its hydrophobicity of amino acid residues within the putative 2nd loop between 140 and 146. These data suggest that emergence of these **HBV** S gene mutants in the phase of **HBV** vaccination program would be most common among populations in whom perinatal/vertical transmission of **HBV** is most common, i.e. southeast Asian and the Taiwanese.

REFERENCE COUNT: 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT